

**From:** [Hawkins, Andy](#)  
**To:** ["Miller, Ken"](#)  
**Subject:** RE: Monitoring  
**Date:** Friday, July 15, 2016 2:02:00 PM

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I think I must have used DNR's

Andy Hawkins

EPA Region 7

11201 Renner Boulevard

Lenexa, Kansas 66219

(913) 551-7179 office

[hawkins.andy@epa.gov](mailto:hawkins.andy@epa.gov)

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**From:** Miller, Ken [<mailto:kenneth.miller@wustl.edu>]

**Sent:** Friday, July 15, 2016 2:01 PM

**To:** Hawkins, Andy

**Subject:** RE: Monitoring

Makes sense. DNR's receptor grid has a lot of duplicates as well; I guess I never checked Ameren's.  
Have a good weekend.

Ken

Ken Miller, P.G.

Environmental Scientist

Interdisciplinary Environmental Clinic

Washington University School of Law

One Brookings Drive - Campus Box 1120

St. Louis, MO 63130

314-935-6368 (phone)

314-935-5171 (fax)

[kenneth.miller@wustl.edu](mailto:kenneth.miller@wustl.edu)

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**From:** Hawkins, Andy [<mailto:hawkins.andy@epa.gov>]

**Sent:** Friday, July 15, 2016 1:56 PM

**To:** Miller, Ken

**Subject:** RE: Monitoring

I believe the difference is my code keeps multiple receptors with the same max value on a day/hour.  
So for example, 15122813 has two receptors with the same maximum. Unfortunately it appears that the receptors\_grid.rou file has duplicate entries and AERMOD output also duplicates these entries.  
So you will find 2 records in the MAXIFILE on 15122813 they look the same...

1 ALL 15122813 674234.5 4259882 188.00 188.00 0 52.70899 674234.49 4259882.08

1 ALL 15122813 674234.5 4259882 188.00 188.00 0 52.70899 674234.49 4259882.08

Then I check the receptor\_grid.rou file and sure enough there are duplicate entries for this receptor location.

DISCCART 674234.49 4259882.08 188.00 188.00

DISCCART 674234.49 4259882.08 188.00 188.00

Your code must remove the duplicates while mine does not.

Anyway, the receptor file should not have duplicates... not sure how that happened... looks like there are 288 duplicates in that file.

Good catch.

Andy Hawkins  
EPA Region 7  
11201 Renner Boulevard  
Lenexa, Kansas 66219  
(913) 551-7179 office  
[hawkins.andy@epa.gov](mailto:hawkins.andy@epa.gov)

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**From:** Miller, Ken [<mailto:kenneth.miller@wustl.edu>]

**Sent:** Friday, July 15, 2016 12:42 PM

**To:** Hawkins, Andy <[hawkins.andy@epa.gov](mailto:hawkins.andy@epa.gov)>

**Subject:** RE: Monitoring

Andy,

Yes, my 10 is at the same location. My 9 and 5 match too. However, I don't have any counts of 4 (see attached), so I wonder if one of us has an error in our code (I'm using VBA in Excel instead of R). My results look OK because my counts add up to 1018, which is the number of unique hours in the MAXIFILE output when using the 30 cutoff. Any thoughts?

Ken

Ken Miller, P.G.

Environmental Scientist

Interdisciplinary Environmental Clinic

Washington University School of Law

One Brookings Drive - Campus Box 1120

St. Louis, MO 63130

314-935-6368 (phone)

314-935-5171 (fax)

[kenneth.miller@wustl.edu](mailto:kenneth.miller@wustl.edu)

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**From:** Hawkins, Andy [<mailto:hawkins.andy@epa.gov>]

**Sent:** Thursday, July 14, 2016 5:09 PM

**To:** Miller, Ken

**Subject:** RE: Monitoring

10 is my max individual receptor count using the 30 cutoff. Can you verify your 10 is at the receptor location highlighted below? That would be a good check for me against a different method like you used.

73 677234.49 4255882.08 4

80 677234.49 4277882.08 4

82 678234.49 4245882.08 4

84 678234.49 4257882.08 4

413 688484.49 4273882.08 5

387 687984.49 4273382.08 9

432 688984.49 4274132.08 10

You can reproduce this from R using your MAXIFILE just change the path in the read.table statement. This code will easily crunch a large output file, millions of lines in short time. And you can modify it to use other cut points or output the counts to a .csv file to plot.

<https://www.r-project.org/>

```
data <- read.table(file="C:\\Users\\ahawki03\\Desktop\\Aermmod thru 12-31-15\\andy3\\andy3.AD\\MAXIFILE_DEF.TXT",skip=9,header=F,fill=T)
```

```
data <- na.omit(data)
```

```
data$loc <- paste(V4,V5)
attach(data)
ag <- aggregate(V9~V3, data, max)
hourly_max <- merge(ag,data,by=c("V9","V3"))
test <- hourly_max[hourly_max$V9 > 30,]
test1 <- as.data.frame(table(test$loc))
colnames(test1) <- c("loc","freq")
test1[order(test1$freq),]
```

Andy Hawkins  
EPA Region 7  
11201 Renner Boulevard  
Lenexa, Kansas 66219  
(913) 551-7179 office  
[hawkins.andy@epa.gov](mailto:hawkins.andy@epa.gov)

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**From:** Miller, Ken [<mailto:kenneth.miller@wustl.edu>]

**Sent:** Thursday, July 14, 2016 4:01 PM

**To:** Hawkins, Andy <[hawkins.andy@epa.gov](mailto:hawkins.andy@epa.gov)>

**Subject:** RE: Monitoring

Thanks Andy. Rasterizing the counts would certainly explain it. And I understand you were looking at all hours, not daily max values – I was too – and that that is not in line with the TAD. Only having 8 months of met data is pretty limiting, so it will be interesting to see what longer data sets with NWS substitution show.

Ken

Ken Miller, P.G.  
Environmental Scientist  
Interdisciplinary Environmental Clinic  
Washington University School of Law  
One Brookings Drive - Campus Box 1120  
St. Louis, MO 63130  
314-935-6368 (phone)  
314-935-5171 (fax)  
[kenneth.miller@wustl.edu](mailto:kenneth.miller@wustl.edu)

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**From:** Hawkins, Andy [<mailto:hawkins.andy@epa.gov>]

**Sent:** Thursday, July 14, 2016 3:46 PM

**To:** Miller, Ken

**Subject:** RE: Monitoring

Ken,

That is likely correct based on looking at your plot and knowing I rasterized the counts. It will take me some time to verify this.

I want to be clear that my method was looking at all hours not the daily max values and does not follow the monitoring TAD. The plot I created was to spur discussion with Ameren and MDNR and to generate further analysis. I will attempt to reproduce your plot by receptor in R.

I may create some R code that can be shared with all parties to post process data following more closely to the TAD.

Thanks for sharing this.

Andy Hawkins

EPA Region 7  
11201 Renner Boulevard  
Lenexa, Kansas 66219  
(913) 551-7179 office  
[hawkins.andy@epa.gov](mailto:hawkins.andy@epa.gov)

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**From:** Miller, Ken [<mailto:kenneth.miller@wustl.edu>]

**Sent:** Thursday, July 14, 2016 3:06 PM

**To:** Hawkins, Andy <[hawkins.andy@epa.gov](mailto:hawkins.andy@epa.gov)>

**Subject:** RE: Monitoring

Andy,

I've attempted to recreate your frequency analysis, but I'm getting significantly lower frequency counts than you (see attached). The highest frequency I get at any given receptor is 10, whereas your highest count is in the range of 30-35. Note that I used the 30 ug/m<sup>3</sup> cutoff, so I'm comparing my results to the figure on page 86 of the Response to Comments document.

I believe I know what the issue is. Whereas I am looking at frequency counts for individual receptors, it appears you are looking at large grid cells that contain multiple receptors and summing the frequency counts of all receptors within each cell. Presumably this is a feature of R, which I don't use and so am not familiar with. Can you confirm?

Thanks,

Ken

Ken Miller, P.G.

Environmental Scientist

Interdisciplinary Environmental Clinic

Washington University School of Law

One Brookings Drive - Campus Box 1120

St. Louis, MO 63130

314-935-6368 (phone)

314-935-5171 (fax)

[kenneth.miller@wustl.edu](mailto:kenneth.miller@wustl.edu)

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**From:** Hawkins, Andy [<mailto:hawkins.andy@epa.gov>]

**Sent:** Thursday, July 14, 2016 11:38 AM

**To:** Miller, Ken

**Subject:** RE: Monitoring

I used the unmerged one. Merged would likely be more appropriate for the reasons you outline below.

Andy Hawkins

EPA Region 7

11201 Renner Boulevard

Lenexa, Kansas 66219

(913) 551-7179 office

[hawkins.andy@epa.gov](mailto:hawkins.andy@epa.gov)

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**From:** Miller, Ken [<mailto:kenneth.miller@wustl.edu>]

**Sent:** Thursday, July 14, 2016 11:32 AM

**To:** Hawkins, Andy <[hawkins.andy@epa.gov](mailto:hawkins.andy@epa.gov)>

**Subject:** RE: Monitoring

Thanks Andy. One quick question – the input file “Labadie\_sites\_default.inp” has units 3 and 4 as separate release points. Did you use that for your analysis or did you use the merged variant “Labadie\_sites\_comb34\_default.inp” instead? The designation TSD says that EPA views runs that do not merge units 3 and 4 as less representative and that treating the flues as one stack better approximates actual dispersion conditions, so I would expect you to have used the latter.

Thanks,

Ken

Ken Miller, P.G.

Environmental Scientist

Interdisciplinary Environmental Clinic

Washington University School of Law

One Brookings Drive - Campus Box 1120

St. Louis, MO 63130

314-935-6368 (phone)

314-935-5171 (fax)

[kenneth.miller@wustl.edu](mailto:kenneth.miller@wustl.edu)

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**From:** Hawkins, Andy [<mailto:hawkins.andy@epa.gov>]

**Sent:** Wednesday, July 13, 2016 11:56 AM

**To:** Miller, Ken

**Cc:** Algae-Eakin, Amy

**Subject:** FW: Monitoring

Ken,

Per our discussion. This describes the process used to create the plots in the pdf Amy shared.

Andy Hawkins

EPA Region 7

11201 Renner Boulevard

Lenexa, Kansas 66219

(913) 551-7179 office

[hawkins.andy@epa.gov](mailto:hawkins.andy@epa.gov)

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**From:** Hawkins, Andy

**Sent:** Friday, July 08, 2016 4:44 PM

**To:** 'Anderson, Kenneth J' <[KAnderson@ameren.com](mailto:KAnderson@ameren.com)>

**Cc:** Michael Jay <[Jay.Michael@epa.gov](mailto:Jay.Michael@epa.gov)>; Peter, David <[peter.david@epa.gov](mailto:peter.david@epa.gov)>; Algae-Eakin, Amy

<[algae-eakin.amy@epa.gov](mailto:algae-eakin.amy@epa.gov)>; 'Moore, Kyra' <[kyra.moore@dnr.mo.gov](mailto:kyra.moore@dnr.mo.gov)>; 'Wilbur, Emily'

<[emily.wilbur@dnr.mo.gov](mailto:emily.wilbur@dnr.mo.gov)>

**Subject:** Monitoring

Ken,

Mike asked that I describe the map he showed on monitor siting. I want to state that map shown was to start the discussion and should not be considered a final EPA approved siting analysis as that was not the intent.

So the frequency overlay represented counts of where on the domain a receptor had a value > 30 ug/m3 and only the maximum receptor domain wide received a count. The modeling used was from your beta request “Labadie\_sites\_default.inp” and I used your onsite met data as provided, so your “KSUSILX-LAB-MIN-A2015D” files. I made no modifications to either the met or emissions inputs and I used your receptor grid “Receptors\_grid.rou” file as provided. I did review your met file and saw no issues. I ran with no background and output a threshold MAXIFILE to output any model result >1

ug/m3 for all receptors, and this output file was the basis of the frequency counts (see R code below). So this approach does not follow the EPA modeling TAD (really can't with only 8 months of met data) and only looks at frequency.

I'm willing to work with you on enhancing this analysis using your onsite met data. It may be appropriate to normalize your emissions and use some reasonable stack parameters with all available onsite met and redo this analysis incorporating frequency and higher concentration combined ranks, I would recommend that for a more robust documented defensible analysis. Someone asked for the coordinates of the monitors...

(38.5818,-90.865528,"NW")

(38.572522,-90.796911,"Valley")

(38.581919,-90.835309,"Quarry")

(38.600896,-90.864733,"Augusta")

I've attached the electronic file I used to map the frequency counts.

And the R code used to create the attached raster... note I made no attempt to find the exact max impact locations just general locations to look at potential monitor sites using more frequent high impacts with your onsite data. I may rewrite my code to redo this analysis following closer to the monitoring TAD even though we have no 3yr average 4<sup>th</sup> highs.

```
#data <- read.table(file="MAXIFILE_DEF.TXT",skip=9,header=F,fill=T)
```

```
#data <- na.omit(data)
```

```
#data <- data[data$V9>30,]
```

```
#attach(data)
```

```
#data <- data.frame(V3,V4,V5,V9)
```

```
#ag <- aggregate(V9~V3, data, max)
```

```
#hourly_max <- merge(ag,data,by=c("V3","V9"))
```

```
#hourly_max$loc <- (paste(hourly_max$V4,hourly_max$V5))
```

```
#counts <- data.frame(table(hourly_max$loc))
```

```
#counts$y <- as.numeric(substr(counts$Var1,10,20))
```

```
#counts$x <- as.numeric(substr(counts$Var1,1,9))
```

```
#counts <- na.omit(counts)
```

```
#plot(counts$x,count$y,cex=count$Freq)
```

```
#counts1 <- data.frame(counts$x,count$y,count$Freq)
```

```
#colnames(counts1) <- c("x","y","Freq")
```

```
#e <- extent(counts1[,1:2])
```

```
#r <- raster(e, ncol=50, nrow=50)
```

```
#x <- rasterize(counts1[,1:2], r, as.numeric(counts1[,3]), fun=sum)
```

Andy Hawkins

EPA Region 7

11201 Renner Boulevard

Lenexa, Kansas 66219

(913) 551-7179 office

[hawkins.andy@epa.gov](mailto:hawkins.andy@epa.gov)